

#14



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/471,459A

DATE: 06/14/2002

TIME: 14:50:24

Input Set : A:\PC10315A Sequence Listing.ST25.txt

Output Set: N:\CRF3\06142002\I471459A.raw

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3 <110> APPLICANT: Pfizer Inc.
4 Fidock, Mark David
6 <120> TITLE OF INVENTION: Enzyme PDE xiv
8 <130> FILE REFERENCE: PC10315AGPR
10 <140> CURRENT APPLICATION NUMBER: 09/471,459A
11 <141> CURRENT FILING DATE: 1999-12-22
13 <150> PRIOR APPLICATION NUMBER: GB 9828603.2
14 <151> PRIOR FILING DATE: 1998-12-23
16 <150> PRIOR APPLICATION NUMBER: GB 9922123.6
17 <151> PRIOR FILING DATE: 1999-09-17
19 <160> NUMBER OF SEQ ID NOS: 26
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 446
25 <212> TYPE: PRT
26 <213> ORGANISM: Mouse
28 <400> SEQUENCE: 1
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31 1 5 10 15
34 Pro Glu Gln Ser Val Lys Cys Val Cys Met Leu Gly Asp Val Arg Leu
35 20 25 30
38 Arg Gly Gln Thr Gly Val Pro Ala Glu Arg Arg Gly Ser Tyr Pro Phe
39 35 40 45
42 Ile Asp Phe Arg Leu Leu Asn Asn Thr Thr His Ser Gly Glu Ile Gly
43 50 55 60
46 Thr Lys Lys Lys Val Lys Arg Leu Leu Ser Phe Gln Arg Tyr Phe His
47 65 70 75 80
50 Ala Ser Arg Leu Leu Arg Gly Ile Ile Pro Gln Ala Pro Leu His Leu
51 85 90 95
54 Leu Asp Glu Asp Tyr Leu Gly Gln Ala Arg His Met Leu Ser Lys Val
55 100 105 110
58 Gly Thr Trp Asp Phe Asp Ile Phe Leu Phe Asp Arg Leu Thr Asn Gly
59 115 120 125
62 Asn Ser Leu Val Thr Leu Leu Cys His Leu Phe Asn Ser His Gly Leu
63 130 135 140
66 Ile His His Phe Lys Leu Asp Met Val Thr Leu His Arg Phe Leu Val
67 145 150 155 160
70 Met Val Gln Glu Asp Tyr His Gly His Asn Pro Tyr His Asn Ala Val
71 165 170 175
74 His Ala Ala Asp Val Thr Gln Ala Met His Cys Tyr Leu Lys Glu Pro
75 180 185 190
78 Lys Leu Ala Ser Phe Leu Thr Pro Leu Asp Ile Met Leu Gly Leu Leu
79 195 200 205

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82 Ala Ala Ala Ala His Asp Val Asp His Pro Gly Val Asn Gln Pro Phe
 83 210 215 220
 86 Leu Ile Lys Thr Asn His His Leu Ala Asn Leu Tyr Gln Asn Met Ser
 87 225 230 235 240
 90 Val Leu Glu Asn His His Trp Arg Ser Thr Ile Gly Met Leu Arg Glu
 91 245 250 255
 94 Ser Arg Leu Leu Ala His Leu Pro Lys Glu Met Thr Gln Asp Ile Glu
 95 260 265 270
 98 Gln Gln Leu Gly Ser Leu Ile Leu Ala Thr Asp Ile Asn Arg Gln Asn
 99 275 280 285
 102 Glu Phe Leu Thr Arg Leu Lys Ala His Leu His Asn Lys Asp Leu Arg
 103 290 295 300
 106 Leu Glu Asn Val Gln Asp Arg His Phe Met Leu Gln Ile Ala Leu Lys
 107 305 310 315 320
 110 Cys Ala Asp Ile Cys Asn Pro Cys Arg Ile Trp Glu Met Ser Lys Gln
 111 325 330 335
 114 Trp Ser Glu Arg Val Cys Glu Glu Phe Tyr Arg Gln Gly Asp Leu Glu
 115 340 345 350
 118 Gln Lys Phe Glu Leu Glu Ile Ser Pro Leu Cys Asn Gln Gln Lys Asp
 119 355 360 365
 122 Ser Ile Pro Ser Ile Gln Ile Gly Phe Met Thr Tyr Ile Val Glu Pro
 123 370 375 380
 126 Leu Phe Arg Glu Trp Ala Arg Phe Thr Gly Asn Ser Thr Leu Ser Glu
 127 385 390 395 400
 130 Asn Met Leu Ser His Leu Ala His Asn Lys Ala Gln Trp Lys Ser Leu
 131 405 410 415
 134 Leu Ser Asn Gln His Arg Arg Arg Gly Ser Gly Gln Asp Leu Ala Gly
 135 420 425 430
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 143 <211> LENGTH: 1341
 144 <212> TYPE: DNA
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 147 <400> SEQUENCE: 2
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 150 gtcaaatgtg tttgcattgtc aggagatgtt cgtactaaagg gtcagacggg gtttccctggcc
 152 gaacgcgcgtg gtccttaccc attcattgtac ttccgtctac ttaacaatac aacacactca
 154 gggaaaatttgcaccaagaa aaaggtgaaa cgactgtttaa gtttccaaag atacttccat
 156 gcatcttaggc ttctccgggg gattatacccg caggccccctc tccacctgtt ggatgaagac
 158 taccttggac aagcaaggca catgctctcc aaagttggaa cgtgggactt tgacattttc
 160 ttgtttgtt gcttgacaaa tggaaacagt ctggtaactc tggatgttca cctcttcaac
 162 tcccatgggc tcattccacca tttcaagctc gatatgggtga ctttgcacag gtttctgggt
 164 atggttcagg aagattacca cggtcacaac ccataaccaca atgtgttca cgcagccgac
 166 gtcacccagg ccatgcacttggc ttacctgtt gggccaaatgtt tggcaagctt cctcacaccc
 168 ctggacatca tgcttgact actggctgca gcagctcatg acgtggacca cccaggggtc
 170 aaccagccat ttttgcataa aactaaccac catcttgcaccc acctgttatca gaatatgtt
 172 gtactggaga atcaccacttgc gcatgttaca atggcatgc ttggagaatc acggctcttg
 174 gctcaacttgc caaaggaaat gacacaggat atcgaacacgc agctgggctc cctcatcttgc

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178	aaagatttga	gactggagaa	tgtacaggac	agacacttta	tgcttcagat	cgccttgaag	960										
180	tgtgctgaca	tttgcatacc	ttgtcgatc	tgggagatga	gcaaggcgtg	gagtgaaagg	1020										
182	gtctgtgagg	aattctacag	acaagggtgac	cttgaacaga	agtttgaact	ggaaatcagt	1080										
184	cctctttgtt	atcaacagaa	agattcaatc	cctagcatac	aaattggttt	catgacttac	1140										
186	atcgtggaggc	cgctgttccg	ggagtggccc	cggttactg	ggaacagcac	cctgtcggag	1200										
188	aacatgctaa	gcccatttcgc	gcacaacaaa	gcccagtgga	agagcctgct	gtccaatcag	1260										
190	cacagacgca	ggggcagcgg	ccaggacctg	gcggggcccc	cacctgagac	cctggagcag	1320										
192	acagaaggtg	ccacgcccata	a				1341										
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196	<211>	LENGTH:	288														
197	<212>	TYPE:	PRT														
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203	1				5							10					15
206	Pro	Asp	Gln	Asn	Ala	Lys	Cys	Val	Cys	Met	Leu	Gly	Asp	Ile	Arg	Leu	
207					20					25				30			
210	Arg	Gly	Gln	Thr	Gly	Val	Arg	Ala	Glu	Arg	Arg	Gly	Ser	Tyr	Pro	Phe	
211					35				40			45					
214	Ile	Asp	Phe	Arg	Leu	Leu	Asn	Ser	Thr	Thr	Tyr	Ser	Gly	Glu	Ile	Gly	
215					50				55			60					
218	Thr	Lys	Lys	Lys	Val	Lys	Arg	Leu	Leu	Ser	Phe	Gln	Arg	Tyr	Phe	His	
219		65				70				75			80				
222	Ala	Ser	Arg	Leu	Leu	Arg	Gly	Ile	Ile	Pro	Gln	Ala	Pro	Leu	His	Leu	
223					85				90			95					
226	Leu	Asp	Glu	Asp	Tyr	Leu	Gly	Gln	Ala	Arg	His	Met	Leu	Ser	Lys	Val	
227					100				105			110					
230	Gly	Met	Trp	Asp	Phe	Asp	Ile	Phe	Leu	Phe	Asp	Arg	Leu	Thr	Asn	Gly	
231					115				120			125					
234	Asn	Ser	Leu	Val	Thr	Leu	Leu	Cys	His	Leu	Phe	Asn	Thr	His	Gly	Leu	
235					130				135			140					
238	Ile	His	His	Phe	Lys	Leu	Asp	Met	Val	Thr	Leu	His	Arg	Phe	Leu	Val	
239		145				150				155			160				
242	Met	Val	Gln	Glu	Asp	Tyr	His	Ser	Gln	Asn	Pro	Tyr	His	Asn	Ala	Val	
243					165				170			175					
246	His	Ala	Ala	Asp	Val	Thr	Gln	Ala	Met	His	Cys	Tyr	Leu	Lys	Glu	Pro	
247					180				185			190					
250	Lys	Leu	Ala	Ser	Phe	Leu	Thr	Pro	Leu	Asp	Ile	Met	Leu	Gly	Leu	Leu	
251					195				200			205					
254	Ala	Ala	Ala	Ala	His	Asp	Val	Asp	His	Pro	Gly	Val	Asn	Gln	Pro	Phe	
255					210				215			220					
258	Leu	Ile	Lys	Thr	Asn	His	His	Leu	Ala	Asn	Leu	Tyr	Gln	Asn	Met	Ser	
259		225				230				235			240				
262	Val	Leu	Glu	Asn	His	His	Trp	Arg	Ser	Thr	Ile	Gly	Met	Leu	Arg	Glu	
263					245				250			255					
266	Ser	Arg	Leu	Leu	Ala	His	Leu	Pro	Lys	Glu	Met	Thr	Gly	Thr	Trp	Asp	
267					260				265			270					
270	Phe	Asp	Ile	Phe	Leu	Phe	Asp	Arg	Leu	Thr	Asn	Gly	Asn	Ser	Leu	Val	

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275 <211> LENGTH: 807			
276 <212> TYPE: DNA			
277 <213> ORGANISM: Human			
279 <400> SEQUENCE: 4			
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282 gccaaatgtg tttgcattgtc gggagatata cgactaaggc gtcagacggg ggttcgtgt	120		
284 gaacgcgtg gtccttaccc attcattgtac ttccgcctac ttaacagtag aacatactca	180		
286 gggagattt gcaccaagaa aaaggtgaaa agactattaa gcttcaaag atacttccat	240		
288 gcatcaaggc tgcttcgtgg aattatacca caagccccctc tgcacctgtc ggatgaagac	300		
290 taccttggac aagcaaggca tatgctctcc aaagtggaa tgtggattt tgacattttc	360		
292 ttgttgatc gcttgacaaa tggaaacagc ctggtaacac tttgtgtgcca cctcttcaat	420		
294 acccatggac tcatttacca tttcaagttt gatatggta ctttacaccg atttttagtc	480		
296 atgggtcaag aagattacca cagccaaaac ccgtatcaca atgctgttca cgccagccgac	540		
298 gtcacccagg ccatgcactg ctacctgaaa gagccaaagc ttgccagctt cctcacgcct	600		
300 ctggacatca tgcttggact gctggctgca gcagcacacg atgtggacca cccaggggtg	660		
302 aaccagccat ttttgataaa aactaaccac catttgcaaa acctataatca gaatatgtct	720		
304 gtgctggaga atcatcactg gcgatctaca attggcatgc ttgcagaatc aaggcttctt	780		
306 gctcatttgc caaaggaaat gacgttaa	807		
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310 <211> LENGTH: 450			
311 <212> TYPE: PRT			
312 <213> ORGANISM: Human			
314 <400> SEQUENCE: 5			
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317 1 5 10 15			
320 Pro Asp Gln Asn Ala Lys Cys Val Cys Met Leu Gly Asp Ile Arg Leu			
321 20 25 30			
324 Arg Gly Gln Thr Gly Val Arg Ala Glu Arg Arg Gly Ser Tyr Pro Phe			
325 35 40 45			
328 Ile Asp Phe Arg Leu Leu Asn Ser Thr Thr Tyr Ser Gly Glu Ile Gly			
329 50 55 60			
332 Thr Lys Lys Lys Val Lys Arg Leu Leu Ser Phe Gln Arg Tyr Phe His			
333 65 70 75 80			
336 Ala Ser Arg Leu Leu Arg Gly Ile Ile Pro Gln Ala Pro Leu His Leu			
337 85 90 95			
340 Leu Asp Glu Asp Tyr Leu Gly Gln Ala Arg His Met Leu Ser Lys Val			
341 100 105 110			
344 Gly Met Trp Asp Phe Asp Ile Phe Leu Phe Asp Arg Leu Thr Asn Gly			
345 115 120 125			
348 Asn Ser Leu Val Thr Leu Leu Cys His Leu Phe Asn Thr His Gly Leu			
349 130 135 140			
352 Ile His His Phe Lys Leu Asp Met Val Thr Leu His Arg Phe Leu Val			
353 145 150 155 160			
356 Met Val Gln Glu Asp Tyr His Ser Gln Asn Pro Tyr His Asn Ala Val			
357 165 170 175			
360 His Ala Ala Asp Val Thr Gln Ala Met His Cys Tyr Leu Lys Glu Pro			
361 180 185 190			

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364	Lys	Leu	Ala	Ser	Phe	Leu	Thr	Pro	Leu	Asp	Ile	Met	Leu	Gly	Leu	Leu
365		195			200				205							
368	Ala	Ala	Ala	Ala	His	Asp	Val	Asp	His	Pro	Gly	Val	Asn	Gln	Pro	Phe
369		210			215				220							
372	Leu	Ile	Lys	Thr	Asn	His	His	Leu	Ala	Asn	Leu	Tyr	Gln	Asn	Met	Ser
373	225		225		230			235			235				240	
376	Val	Leu	Glu	Asn	His	His	Trp	Arg	Ser	Thr	Ile	Gly	Met	Leu	Arg	Glu
377			245			245			250			250			255	
380	Ser	Arg	Leu	Leu	Ala	His	Leu	Pro	Lys	Glu	Met	Thr	Gln	Asp	Ile	Glu
381		260			265			265			270					
384	Gln	Gln	Leu	Gly	Ser	Leu	Ile	Leu	Ala	Thr	Asp	Ile	Asn	Arg	Gln	Asn
385		275			280			280			285					
388	Glu	Phe	Leu	Thr	Arg	Leu	Lys	Ala	His	Leu	His	Asn	Lys	Asp	Leu	Arg
389	290		290		295			295			300					
392	Leu	Glu	Asp	Ala	Gln	Asp	Arg	His	Phe	Met	Leu	Gln	Ile	Ala	Leu	Lys
393	305		305		310			310			315				320	
396	Cys	Ala	Asp	Ile	Cys	Asn	Pro	Cys	Arg	Ile	Trp	Glu	Met	Ser	Lys	Gln
397				325			325			330				335		
400	Trp	Ser	Glu	Arg	Val	Cys	Glu	Glu	Phe	Tyr	Arg	Gln	Gly	Glu	Leu	Glu
401		340			340			340			345			350		
404	Gln	Lys	Phe	Glu	Leu	Glu	Ile	Ser	Pro	Leu	Cys	Asn	Gln	Gln	Lys	Asp
405		355			355			360			360			365		
408	Ser	Ile	Pro	Ser	Ile	Gln	Ile	Gly	Phe	Met	Ser	Tyr	Ile	Val	Glu	Pro
409		370			370			375			380					
412	Leu	Phe	Arg	Glu	Trp	Ala	His	Phe	Thr	Gly	Asn	Ser	Thr	Leu	Ser	Glu
413	385		385		390			390			395				400	
416	Asn	Met	Leu	Gly	His	Leu	Ala	His	Asn	Lys	Ala	Gln	Trp	Lys	Ser	Leu
417				405			405			410				415		
420	Leu	Pro	Arg	Gln	His	Arg	Ser	Arg	Gly	Ser	Ser	Gly	Ser	Gly	Pro	Asp
421		420			420			425			425			430		
424	His	Asp	His	Ala	Gly	Gln	Gly	Thr	Glu	Ser	Glu	Glu	Gln	Glu	Gly	Asp
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442	gaacgcccgt	gtccctaccc	attcattgtac	ttccgcctac	ttaacagtac	aacatactca									180	
444	ggggagattg	gcaccaagaa	aaaggtgaaa	agactattaa	gctttcaaag	atacttccat									240	
446	gc当地caaggc	tgcttcgtgg	aattatacca	caagccccctc	tgcacccgt	ggatgaagac									300	
448	taccttggac	aagcaaggca	tatgtctcc	aaagtggaaa	tgtgggattt	tgacattttc									360	
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454	atggttcaag	aagattacca	cagccaaaac	ccgtatcaca	atgctgttca	cgcagccgac									540	
456	gtcaccagg	ccatgcactg	ctacctgaaa	gagccaaagc	ttgccagctt	cctcacgcct									600	

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